

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USN 09/081,385
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTG CTTTCCTTCC CGGGGAAAGG CCGGGGCCAG AGACCCGCAC TCGGACCAGG	60
CGGGGGCTGC GGGGGCAGAG TGGGCTGGGG AGGGCTGGGA GGGCTCTGG GGCGGGCTCC	120
TCCAGGCTGG GGGCCCGGAG CTCCGGGAAG GCAGTCTGG CCTGCGGATG GGCGCGCG	180
TGGGGCCCGG CGGGGCCGCC TCAGGAGGCG TCCAGGCTGC GGGAGCGGGA GGAGCGGCCG	240
TGCGGGCGCC AGCGCCGTGG GTGGAGGTG CCGTCCCTCC TGAGGGGAG CCAGTGCCTT	300
TGGGACCCGG GAGCAGAGCC CGCGCCCTCCC CAGCGGCCCTC CCCGGGGGTC TCAACGGGTC	360
ACCCGAGAGC GGAGGCCCG GCTCCGCAGA AACCCGGGGC GGCCGGGGGG AAGCAGCGCC	420
CTCAGGCCGTC GGAGGAGGCC CCAGAAGGAC CTCCGGCTCT CCCGCCGGGC TCCGACCGCC	480
TGGGTCGGT CGGGGACGGC CCAGGCCGCC AGAACCCCA AGCCAGCTC AGTCTGCAGG	540
GCACGACCCA GAGGCCACCA GCAGAGGACG GGGCCGGGGC CGGGAGAGGG CGGGGAGGGC	600
GCTCCCTGGGA GGTCAAGGCC AGGGCTAGAC TTTCAGGGTC ATGGCCTGGC CCCTCATCCC	660
CAGGGAGGTG AGGGGGCTCT GTGAGCAGAG GGGGCCCGG TGGAGAAGGC GCTGCTAGCC	720

AGGGGCGGGG	CAGGAGCCCA	GGTGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AAGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TGCTGCCGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTCAG	900
ATTTCAAGGA	GTTCAGGTG	GAGACAAAGG	CCAGGCCAG	TGAAAATGT	GGCAGTGACA	960
GAGTATGGG	TGAGAACAC	GGAGAGAGGA	AGTCCCCGAG	GGCGATGATG	GGACAGAGAG	1020
CGGGGACAG	AATTTTAA	AACGCATCTG	AGATGCGT	GGCAGACTCA	TAGTTGTTT	1080
CCTTCACGG	AGAAAGTGTG	GGCAGAACCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTCCCTC	CCTGTACAC	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCA	GGAAAGCTG	ATCCGCCCG	ACCCAGGGCC	1260
CCCCGGTGC	CCCTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAAC	1320
CCGGACACGG	GTCGTGTGCT	GCACCTGGCA	GTTCAGGAC	CGACACCCAC	AATGCTTAA	1380
GAGGTATGA	CTGCCTTCCA	GGGGCCTGGC	TGCTGTGACAC	TTGCTATGGC	TCCTGGAGAA	1440
GAGGGATTGA	TGAGGAGTC	GGGGCATGG	CACGTCCTG	GGTGTGCT	CTGAGGCAAG	1500
GCCCCGCTGG	GGTGAAGAAGG	GGCTGGAGAC	AGGTTCTGC	CAGTTCAGCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAACC	CACTGGGGC	TTATGAAACT	GCAGGTTGCT	GAATCCTTG	1620
CATGGGGTCT	CTCCTTCAGG	AGGCTGGGT	GGGGCCTGGAG	ACTGTACCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGATGTGGC	CTGGCCTGT	GTGGCTCTG	ACCTAGTCCT	TGGGCTTGGG	1740
CTGGCGCCA	GGGCTGGGC	TTAGAGACAGC	TGTGACGAG	GCAAGCATT	TACCCGTT	1800
GTGGGACAT	TACATCTTC	TAGCTGGAA	CACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
TCCTCTCCA	TGTTCTCTC	TTGAGAACCT	TTACAGGTA	TGTCAGGAGC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGAAA	GCCCTCATCC	TTGTCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GCGATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAATCG	AGACAGCTTC	CTGGAGGCG	TGACACCTG	ACAGGGCTT	CCACAGGAGG	2100
AACCGAAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGAAACA	GTGCGCGCAG	2160
AACCAACAC	CACCCACCC	CTAGGCCCAG	AGCTCACCGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCTCTG	GGATCTTAGG	TCTTGTCTT	GGCAGCTCT	GCTGAGACCT	2280
CTATGCCCTG	TCCAGGCTGC	ACCAAGGTT	TGTGACTATT	GGTCTGGGGT	TGTTTGCAAG	2340
CAACTGAAGT	GTTCGTGTTG	AAAACAGGCA	CTTGATTTCG	TGGAAGGAAT	GCTGTTGTT	2400
CTTGTGCGA	CAAACATTGA	GCAGCATTAA	GTGGGCGGTT	TATATCTTG	GGAGTAATGG	2460
GTGTTTTG	AGTCTGTCT	GGGTACTGCA	CATTTAAAGG	AAATCATTT	TCTGAAACAT	2520
TGCTATTTC	CACACAGAA	ATCATATCT	CTTGCTGGTC	CATGTCGAA	GACCTTACAC	2580
GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAACTAATT	ATATCATA	2640
TTGCCGCTT	CTCACTCTGC	TCTTTTCTAT	CTTGTCTAA	TTCTCATTTT	TTCTGCTTCT	2700
TTTGTGTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTG	AAACATCTCGA	GGTGTGAAAC	2760
AAGTAGAGA	CTGAGATTG	AGGATTAAG	GTGGTCTTGA	GCCTTCTAGG	GTTCTTCAC	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCTCA	2880
TTGTTGAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGAC	CATGTTGAGG	TAGTCCTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCA	3000
AAACTTATT	ATCATGATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
CTTGTGCA	CTGTGGATG	TTGTGTAA	TTGAAGGATG	GGAAATGTC	ATGATCTG	3120
CAGGGCTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAAATCTGT	3180
TCCCAGACT	TGTCGTGCT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTT	3240
GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAAT	CTGAAAGAAT	TTATACTGAG	3300
ACATCATCAT	TCCACTTTGT	ACATATCTG	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360
GAECTCTGC	CAGGACCGCC	TGCAACAAAGA	CTGGTATGTC	ACCTCTGGG	TCATCACTGC	3420
CAAGGTTATC	TTCCTAACTCT	ATGTGATCTG	TTGATACCTG	GTGAGGCTA	TGGACAAGCT	3480
GTAAACCAA	ATTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTCT	GCTATTCTG	3540
CATTAAGAG	AAAGCTCTT	GTAGTTGTAG	CAGGTAAGG	AGATGGAAGA	GGCAGCTGGT	3600
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGACA	TGGGGCATAT	3660
CCCCATTCTAT	CTCTGATTTC	TGGAATGGT	TTGCCATAAA	AAGTACTTAG	TTCAGGTGCC	3720
AGCTGTCTT	ATCTCCATT	TCCCAAAAC	TGGGCGAAC	GGCGTCTGAA	TCCAAGGGGA	3780
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCGG	GAGGGGGGGC	GGCTACGGCT	3840
CCTCTTCCGT	CTCCCTAGTG	CGGGGAACT	GTAGAGCCG	GGGGAGACCA	GCCGAGAAGA	3900
CAAATCGTTG	CTTCTCTTC	CTCCCTCTCC	TCCCTCTCC	ACATAGAAAC	ACTCACAAAC	3960
ACCCGACAC	GGGCCGGAGC	TACCGGGGGG	GCATCGCCGC	GGGGCCGGGA	ACCAATTCTC	4020
CTGTCGGCGG	GGGCGTCTT	TGGATCC				4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAAG	GTCAAACCTCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCGC	GCCCCGGCCGG	60
CGCGCGGCGG	GGCGCTTGGC	GCCAGAACGG	AGAGCCCCCTC	GGGGCTGCC	CCCCCGCCCTC	120
ACCGGGTCA	TGAAAAAACG	ATCAGAGTAG	TGGTATTTC	CCGGCGGCC	GCAGGGCCGG	180
CGGACCCCCG	CCCGGGGCCCC	TCGGGGGAC	ACCGGGGGGG	CGCCGGGGC	CTTCCCAC	240

TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCCGCT	GATTCCGCCA	AGCCCCTTCC	CTTGGCTGTG	GTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCA	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTCA	TAGTTACTCC	CCCGCTTAC	CCCGCGTTCA	TTGAATTCT	480
TCACTTTGAC	ATTCAAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
TTCGCGATGC	TTTGTGTTAA	TTAACACAGTC	GGATTCCCT	GGTCCGCACC	AGTTCTAAGT	600
CGGCTGCTAG	GGGCCGGCCG	AAGCGAGGCG	CCGCAGCGAA	CCGGGGCCCC	CGGGGCGGAC	660
CCGGGGGGGG	GACCGGGCG	CGGGCCCTCC	GGCGCTGCG	GGCGCCGCG	CCGCCCCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGCAGCA	GGGCCCCCGG	GTGCCCGGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCCGCG	GGGGGCCCCG	CGGCCGGCCG	CCGCCGGCC	CTGCCGCCCC	GACCCCTTC	120
CCCCCCGCG	CGCCCCCACG	CGGGCTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCAGGGG	180
AGAGAGAG	AGAGAGAGGG	CGCGGGTGG	CTCGTGCAGA	ATTCAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG	AATTGGCAC	GAGGTAGTCA	CGGCTTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTA	GTTGAAAAA	GTGATGCCG	ACGGTGCAGC	AGGCCTTGT	GATGTTCTGC	120
CCGTCAGCG	ACAGCTTGGC	GTGCTGGCG	CTCACGGGT	CCGCATACTG	CAGCAGGGCC	180
TGGAACTGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTCGCAA	CTTGGAGAAA	240
ATCTGGTGC	GCACATCCAG	GTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCGGGCCAT	GCACATCCCT	GCATCCACGG	CCGCCGCCGA	GGCAGCCAAG	360
GCCAGGTTCC	CGGACTGGAC	CGAGTTCACC	GCTGCAGGG	CCGCCTGGC	CCGCGCTGG	420
TTGGGAGAGC	TGTCGGTCTT	CAGCTCCCTG	TGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
CCGGCGAGCA	CAGGGGTAC	CGAGGTGTA	TAGTCACCA	TGGATTGGC	AGCCTCCCTC	540
GTGTTCATCT	CGATGAAGGC	CTGGTTTTC	CCCTTCAGCA	TCAGGAGGT	GGTACCTTC	600
CCAAAGGCCA	GCCGGAGGG	GATGACTTCC	CCCTTCGTA	CTGCGATGGG	GAGCTCCGG	660
ATGTGGATCA	CTCTAGAGGG	GACCGCTGCA	CTTCGGCTGT	CACCTTGAA	CTTCTTGTG	720
TCATTCCTG	TTCCTGAGA	AGCCGAGTTG	CTGCTCATGA	AAACGGTCC	GTTAGTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCG	TTTGACCAA	CGGGTATATA	TGGGACAATG	840
CCGGCCATGG	CACACAGAC	AGACCCCGCG	GGGACGGAGT	GGAGGCCCG	GAATCTTGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTCGTGA	GACGAAGCGC	AAGATGAGA	GTGCTTGTCA	960
GCTGGGCCCT	GCACTGACAG	CCCACCTCTA	CAGCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCCTT	GCTGACCTCA	GCCAGAAGTC	CCCAGAGCTT	CAGGAGGAAT	TTGGTACAAA	1080
TGCAAGACACAGAA	AAACAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTC	ACAATGCTGT	1140
CTTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
GAAGACAGT	GAGGCTGCCA	GGCTGGAATA	TGATGCTAC	CGAACACAGT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTCGACTT	GAGAGTGCC	AGGCCACTTT	1320
CCAGGGCCCAT	CGGGACAAGT	ATGAGAAGCT	GGGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAAGAA	AAACAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTC	ACAATGCTGT	1440
GTCCGCCTAC	TTTGTGGGA	ACCGAAACAA	GCTGGAGGC	ACCCCTGCAGC	AGTTCAACAT	1500
CAACCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCTGGCTA	GAGGAGCA	GAGCTGCTCC	1560
CAGCCCAACT	TGGCTATCAA	GAAGAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCCTTGT	CACTTGCCT	CTGGCTTGGG	CTCCCTTTC	TGGCTGGGGC	1680
CTGACACCAAG	TTTGCCCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAGTTG	1740
CTGGCCCTGTC	TATCTTCTG	GCCACAGGGC	TTCATTCCTCA	GATCTTTC	TTCCACCTCA	1800
CAGCCAACGG	CTATGACAAA	ACCAACTCCCT	GGCCAATGGC	ATCACTCTTC	AGGCTGGGGT	1860
GTGCTCCCTG	ACCAATGACA	GAGCCTGAAA	ATGCCCTGTC	AGCCAATGGC	AGCTCTCTC	1920
GGACTCCCCCT	GGGCCAATGA	TGTTGCGTCT	AATACCCCTT	GTCTCTCTC	TATGCGTGCG	1980
CATTGAGAG	AAGGGGACTG	GGACCAAAGG	GGTGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

CCTTGATCT	GAATAGGCCT	ACCCCTACCA	TTTATTCACT	AATACATTT	ATTGTGTT	2100
TCTAATTAA	AATTACCTT	TCATCTGCT	TGATTTCT	TCAGCTAAAT	TAGAAATTG	2160
TAGTTTTCC	CCTAAAAAT	TCATGGCAT	TCTTCTTAT	AAATTACATT	CTCTGATTT	2220
CTTGTAGCC	TGCTTAAGG	AAATCATGT	GTCAAAATG	CTTGCTCGCA	GTTGCTCCA	2280
TACCAAATGG	TTGCTAAC	CAAATATCTG	AGCAGCAAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAAGTACGGT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCACA	CATCCTGAAC	2400
TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCACTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCG	CACTGCCACA	AATACAGTAG	GAATGCCATC	2520
CCCTTACATC	TCAGCTTAA	TCCTCAGAT	TCATCTGGT	CCTTATGCG	CAGATGTTAC	2580
TCGAAGTCA	CATGAAATGC	CAAATTTCC	ACAGGCCCTC	TTGATTTTT	CACAGTGA	2640
AAGATCAGAA	GTAGAGCCAA	TCAACACTAC	AACCTGAC	TGACTTTCTG	ATTCAAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTAAA	TTTTTTCTT	ACCATTGGG	GCCCTTCAGG	2760
AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTGTCTTC	TGTTGGCTC	GATCTCTGA	2820
TGGCCAGAGT	CTCAGGAAT	CATTGTCAT	AACATCAGCA	AGAACAAATT	CTTGGTGGT	2880
TACATCAACA	CCAAATCAA	TCTTCATATC	AACCACTGTA	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCCAGT	ATTTCAAATA	TAGCCTGTG	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTG	TGAAAACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCCGCC	60
CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGAC	GCAGGAACAT	GGGCTGACT	CACGACAACA	TTGAAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCTC	CCGTCCCCCG	AGCCTGGCC	CACCAAGGTC	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAACAGGAC	300
AAGAAAGGAA	GGAGATTGGA	AGGAGGGAG	AAATGGGTC	CCCGACTGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAGCT	TCCCATGGAC	AGGAGAGAGA	AGGGAAAGGG	AGAGGAGAGG	TTTCCCTCA	480
ATCCCACCCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TCGTCACCC	CTCCCCAACAA	540
CAGTGAATGC	TAAGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGCCCC	600
CTTCCAAGC	CAGGCCACCTC	CAGTGAAGG	GGCACACAG	GAGCATGACA	GCCAGAAAGT	660
GAGGGATGGG	GGGGCGGGGG	AGGGGCAAGG	CGGACTCCAG	AGGGCCCGT	GGGGTTTTGA	720
AATGAAGGA	GGACTGGTC	TGAAGCCTCT	CTCCCTCTG	GTCTCTGT	TCCCCAGAAAG	780
TCCCTCTCCC	ATGTCTGGAG	TGTCTGTTT	ACCAAGGCG	AATCCCCCT	CTGCGTGGG	840
AGAGGGTAG	GCCTTAGTAG	CGGTGTGGG	GGGTCTCGAT	GATGCGTCTC	TCGTCGCTG	900
TGGGGAATC	GCCACACCTC	GAGTCCTGTC	TGCTCTCATC	CTCTGCTG	CCCCAACAG	960
CCCCCTGCA	ACAGGACTGC	CGATTCTGGT	AGGACTCCAT	GGGGTTACA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCTAGAA	AGGTCTGGT	CCTTGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACGCGG	CGGTGAAGGG	AATGGATGCC	CACCAAGGCC	AGGACGACCA	1140
TGAGCACCAG	GAAGCCCACG	CACACCAAA	TGATGAGGGT	TGCGCCGCTG	GGTATCATGG	1200
AGTTCTGTG	GGAGCTGGCT	AGGCTGTGTC	CAGCCATCTC	AGGCGGGGGC	TGGTACAC	1260
GGTGCAGGAA	CTGCTGGGAG	CTGAGCACGT	GGCTGGGGTG	GGCAACCCGG	TTCATGCTGT	1320
GCAGGACATT	GACCTCCACC	ATGAAATTCA	TGCTGGAGTA	ACGGCCATT	ATTTCCGAGC	1380
AGGAAAGCCG	GAACTTCTG	GTGTAGAGGG	CAGCTCCGTG	TCGCAAGCGA	TAACGGCCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGTATG	TCTCCACCCC	AGCAATAGT	AGGTAGGCCAG	1500
ATGTTGTTGGT	GGAGCTGGC	CCCCGCTGCT	CGAGAGGGT	TGTTCCAGG	AGCAGGCC	1560
CCCGCTCGG	ATCCAGGTCA	CCCCCCACCA	GAGAAATTTC	ACAGCCATCC	AGGTTGTGCA	1620
CAACTCTCATC	CGACATGCGT	GTGTCTGTCA	CTGTGCCCTG	CCAACTCTCA	TCCCTTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGGAAACAA	GGGACGCCGT	1740
TGGTCCCTC	AAAGTCCACA	GCTGGGGGG	AAAATGAGC	AGTCCACCTC	AGCAGGATCT	1800
GGGGGGCGT	AGGCTGAAGG	ACGACCACGT	AGCCCCTCAC	TTCAGGGATG	GAGACGCC	1860
ACTCTCGCT	GAAGCACTTG	ACAGCTGTTG	TGAGGCCAG	GGGCGCTGAC	CGGGGGCGTGG	1920
CAAAGCGAG	AGTGTTCATG	TAAGCCACAT	GCTGCAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGAAGC	AGGGACTGTG	AGGGGTTCAC	GTGGACCTTC	ATGCCCTTGC	2040
CCAGGCTCTC	GAATCCCTA	TAGTCCAGCC	CCTCCCGACA	TGCACTAGGG	CACTCGATGA	2100
CCTCGGGCT	CTCCAGGGCA	CCTGAGCGCA	CGCTGAACAC	AGCCAGGTAG	CCATGGAAGT	2160
AGTGGTGGAT	CGACAAAGGG	TCTCTTGGG	TGGTGTCTG	ACTGTTGTCT	CCCTTTCCCT	2220
TCTCTTGGT	CTTCTCCCTCA	GTCCAGCAGG	CCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGTGGAT	GAGGCCATTG	TGATGGATGA	GGCAGGGTC	GAAGGAGATG	CCGTCGGTAT	2340
AGAGTGTGAC	TGTGGGGAAC	TCGAGGTTC	GAGCGTAGTG	GTGCCACT	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACTTGACTG	GGCGGGCAGT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAAGCAAT	CTACACGGCG	TGGACAGTC	GCGAGTAGTG	AGAGAAGGCC	TCCTCATTCT	2520
GGACAGTGT	ACATACGATG	GTTCCTCTT	CCTTCTTGGC	CTTGTGGGA	GTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGGT	CACTGAGGCT	GTCCCTGGGC	CCAGACCCCA	2640

GCCCACCTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCCTGTC	CTGGCTGTAG	TGCAACCGAGA	GTCTGCTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCCACA	GAGTTCCCG	AGCGCCCGCT	2820
CTGAGTAGTT	GTCACCGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAAGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTCA	TATTCGATCC	TTTTGTTCCA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGCTT	CACCTGAATC	TCCACCTCGAG	CATCATCTGC	TGCCCCGCTTC	TTCCCACAGT	3060
CATAAGCTGT	CACTGAAAC	TTATAGAGCT	TCTCACCACT	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCCTCT	GTACACAGCGC	CACGATACAG	CGGTTCCACA	AACACTGGGG	3300
CAAACCTGTT	CACATCGTTG	ACCCGACATC	GCACAGTGGC	CTTGGGGAC	TTCTTGGGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCCCTGGAT	GGTGAAGGTG	TGTTCCCTCT	3420
GGGCCCCGTC	GTCCACAGGC	TCTCTGGCCC	GGATCAGCCC	CTCTCTGTG	GCCTTGCAA	3480
GGATCACAGC	CTCAAAAGGC	ACCCCAGACCC	CATGGAGCCG	GAAGCCGAG	ATCTCACCTG	3540
CATAGGGCAG	CGGGGCATCC	TTGTCAGG	CAAAGAGTGG	TGGATTCAAGT	AGGACCGTGT	3600
TGTCAATTCTC	CATGACGATG	CCCTGGTACT	CTGCCTCAAT	CCATGGCTTG	TGCTTGTGTTG	3660
CTTTGTATACA	GGAGCAGGAC	GGCAGCAGAC	AGGCCAGCAG	AAAGGGCAGC	AGCAGGAGGG	3720
TCATGGTGCG	GGCGGGGGCA	GGCGAGGGGCC	AGGCCTTGC	TCCCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTG	CACCTTGCGG	GAGGGATAACA	GGGGGGGGAA	ACCAAAATAA	AACGTCAAAT	3840
AAATTGTTGA	GGAGGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CGAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTTCAAG	GATCACTGCT	GCCACCCACCG	CCACCCCTGGG	AGCCAGTTAT	3960
TTTGCATGG	CCTTGATTGC	AACAGCTGCC	TCCTCTGTCA	TGGCAGACAG	CACCGTGTAC	4020
AGGATCTCTT	CTCCACAGTC	GTACTCTGTC	TCATCTCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCTGGAGCA	GTGATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAG	ATTCGGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCCCAG	CCCAAGGCTC	60
AGAACAAAGC	GAAGCGTTGC	CTCTTTGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAAGCCC	120
CTCCCCCTGCA	CCCCCCCCAG	CAGTCATCA	GAATGAAAGGA	GGAGCAGTAC	CTCGGGCACG	180
AGGGTCCAGG	AGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCTCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTCTGTG	GTGTATGGC	CTGAGCGGC	CTCACGAGCC	ATGETGTCCC	300
AGCAGGGTGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGG	TGGGGGTGTC	AGTACAGCA	GCTGGCAGGC	CGAGCAGGCC	CAGCCTCCAC	420
CCCATTCAAC	ATGGAACCTG	CACAGTCCTG	CCCTCTACAG	TGCAACCAAG	GGGAGCCGC	480
ATCCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCCCTGA	GGCACAGAAG	CGGGAGAAAAG	540
CGGGGGGCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGC	CCCCCTGAATT	CTTCCCACAG	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCG	CCTGCAACCC	TTCCAGCTGG	CATTCCGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCCGCC	CCAAACCCGG	TGGCTGCCCT	CCCTCCACAG	AAGCAGCAGC	780
AGCACCGAGCA	ACACACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCCCTGCA	GCAACCCAG	GACTTTGGCC	900.
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTCGCACAA	GGCCCTTCTG	CAGGACTCTG	1020
CCCCCGAGCG	AGCGCTACCT	CAGGTCCAGA	TCCCCCTCCC	CCGGCCGCTCC	CGCCGCTCT	1080
CTAAGGAGGG	TATCTGCTC	CCCAAGCGCC	TGGATGGGGC	TGGCACCCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTT	CTACATCACT	GGCCCCCTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCGTAA	GCTCTGGGAT	TCCCCTGGA	GCTGAGGGAG	TCCGAGCTAC	1260
TGCCTGATGG	GGAGAGACTA	GCACCCAACT	GGCCGGAGGC	AGAGGCTCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCAGAC	GGGACTGTGG	CGAGGTGCTA	CGGGCCGGAG	1380
TGATCCAGAG	CACCGCAGCG	AGGCCCGGG	CATCCAGGA	GGCCAATTG	CTGACCCCTGG	1440
CCCAGAAAGC	TGTTGAGCTG	GCCTCACTGC	AGAATGAAA	GGATGGCAGT	GGTCTGAAG	1500
AGAACGCGAA	AACTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTT	TCTGAGCCTT	1560
CCTTAGGCC	CAAGCGAGCA	CGAGAAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGCTGT	GCGAACTGTG	GACCCAACTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAC	AACCCCTGCTG	AGCACAAAGCC	ATCAGTCATC	GTACCCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGG	GCCCAAGGCC	GAGCCCCCTCA	1860
TCATCCCCAC	CAAGGCGGGC	ACTTTCATCG	CCCCTCCCGT	TAECTCCAAAC	ATCACCCCAT	1920
ACCAAGAGCCA	CCTGGCCTCT	CCCCTGCGCC	TAGCTGACCA	CCCCCTGTAG	CGGAGCTTG	1980
AGCTACCTCC	CTACACGGCG	CCCCCCATCC	TCAGCCCTGT	GGGGAAAGGC	TCTGGCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAAGCACCA	TCCCTGCCCC	TCCTCCCAC	ACGCCATAAGA	2100
GTGCCCATCG	CACCGTGTCTC	CGGACTAACAA	GTCGTAAGT	AACCCCGCCT	GTCCCTCTG	2160
TGATGGGGGA	GGCCACCCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGGC	TCCCGGTTCC	2220
AGGCAGAAAT	CCCCCTGATG	AGGGACCGTG	CCCTGGCAGC	TGAGATCCC	CACAAGGCTG	2280
ACTTGGTG	GCACCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAACGAG	AGGAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTCCCTGG	TGCTGGCACC	AACCAAGGAGC	2400
TGGCCCTGCA	CTGCTGAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	ATAAAGCTGC	2460
TGCTGAAGAA	GCCCTGCGG	CCCCACAAAC	ATCCGCTGGC	AACTTATCAC	TACACAGGCT	2520
CTGACAGTG	GAAGATGGCC	GAGGAGAACG	TGTTAACAA	AGGCATTGCC	ATCTACAAAGA	2580
AGGATTCTT	CCTGGTGAG	AAAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAAG	CAGGTAAAAA	TGGGCCCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAAGTCGGCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCCAAAGTT	CCCAAGGGTG	CCTCTCCCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCAAAGAG	GGAGGTGAAAC	GAGGCCAGGA	AGGAGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCCAG	AGCGCAGCAG	GGGGCAGCG	GCAGTCAAAG	2940
CCACCGAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTCAG	AAAAAAAAAA	AAAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTGGCA	CGAGGTCAGT	TTCTGTGGA	ACACAGAGGC	TGCCGTGCCC	ATTCAAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATAA	GGGATCCAA	CAGTGGATT	GTGTTAAC	120
TTAATCCGCT	AAACAGTTCG	CAAGGATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTATGT	180
TTAATGTCG	CGGACAATCG	CCTGTCGTG	GGACCATCCT	GGGAAAACCT	GCTCTGGCT	240
GTGAGGCGAGA	AACCCAAACT	GAAGAGCTA	AAATGGAA	GGCAGCAAGG	CCAGTCGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTA	TCGTCGGCTT	TGTTTGAAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATT	CTGCATCAAG	ATATCGACTC	TGGCAAGGG	ATCCGAAACA	480
CTTACATTG	GTGTTGAAACC	GGCGTGGCT	GTGTTCTTC	TCCAGTGGAC	TGCCAAAGTC	540
CCGACCTGGC	TGAAATGAG	TACGACCTGA	TCGGCTTAAG	CACAGTCAGG	AAACCTTGG	600
CGGCTGTTGA	CACCTCTGTC	GATGGAGAA	AGAGGACTTT	CTATTGAGC	GTTTGCATC	660
CTCTCCCTTA	CATTCTGGA	TGCCAGGGCA	GGCGAGTGGG	GTCTTGCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTCAGA	TGAGTCCCCA	AGCGGGGGCA	AATGGATCTT	780
TGACCATCAT	GTATGTCAC	GGTGACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTGAGTG	TGCTCAGATA	TGGGGCTCAC	CAGCATTCA	GCTTCAGGAT	GGTTGTAGT	900
ACGTGTTTAT	CTGGAGAACT	GTGGAACCT	GTCCCCTGT	CAGAGTGGAA	GGGGACAAC	960
GTGAGGTGAA	AGACCCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTCTC	1080
CAGACGCTG	CCCCACAAAGT	GACAAGCTCA	AGGTGGCTC	CTCATGTCAG	AAAAGCCGG	1140
AACCCGAGG	ATTCAACAA	GTGGCAGGTC	TCTGTACTCA	GAAGCTAAC	TATGAAAATG	1200
GCTTGTAA	AAATGACTTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTAT	CAGCGCTCCA	1260
CAGGCACTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTCTA	AAGGAGACTT	1320
CAGATTGTT	CTACTTGT	GAGTGGCGAA	CCGAGTATGC	CTGCCCACTT	TTGATCTGA	1380
CTGAATGTT	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTC	CTGTCAGGT	1440
ACAGTGCAC	CTGGGAAGCC	ATCACTGGGA	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGGCCCCG	CAGGCTGGCA	CTGAGCGCTG	CCCTCCAGAA	GCAGCCCGT	1560
GTCTGCTGG	TGGCTCCAAG	CCCGTGAACC	TCGGCAGGGT	AAGGGACCGA	CCTCAGTGG	1620
GAGATGGCAT	ATTGTCTG	AAATACGTTG	ATGGCGACTT	ATGTCAGAT	GGGATTCCGA	1680
AAAAGTCAC	CACCATCGGA	TTCACCTGCA	GGCAGAGGCC	AGTGAACCTC	AGGCCCATGT	1740
TCATCAGCG	CGTGGAGGAC	TGTGAGTACA	CCTTGGCTC	GCCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTGACCAA	CCCAAGCACA	GGACACCTGT	1860
TTCATCTGAG	CTCTTAAAGT	GGCAGGGCG	GATTACAGC	TGTTACAGC	GAGAAGGGT	1920
TGGTTACAT	GAGCATCTGT	GGGGAGAATG	AAAACGCC	TCTCGCGTC	GGGGCGCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGG	GCTGAGATAC	GTGGCCAGG	2040
TCTCTGAGCT	GGTGTACAAG	GATGGGCTCC	CTTGTCCCT	CAAATCCGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTCTGT	TGCAGGGCTG	AGGCGGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACTCTCT	TCTTCTCTG	GCACACGCCG	CTGGCCCTGCG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCAT	TGTTGACTTG	TCTCCCCCTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTG	GGATGATGCC	TCCGATACCA	2340
ACCCGTATT	CTACATCAAT	ATTGTCAGC	CACTAAATTC	CATGCAAGGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTC	AAAGTTCTA	TTGATGGTCC	CCCCATAGAT	ATCGGGGGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATG	CAAATGAGAT	TTACTTGAAT	TTTGAAGCA	2520

GTACTCCTT	CCAGGAATT	C AGTTGAAAT	A AAAATTGAAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAAGCTT	TAATTTTAG	GGACTGAAA	CAAGGCTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACTCTTA	TGTTCTTAG	GCTTGTAAAT	ATGTGAGGA	ATATATGGAT	ACTGAGGGAG	2760
TCACAAATT	GGTCTCCACC	AGTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAC	2820
TCCATCCTGA	CGACCCAGTA	TCTCTGTCA	TAAGCCTTT	ATGCCCTCAA	CTTCATCTC	2880
TCCTGGGTTA	AGTTCACAC	CAGGTAGTT	GAAGAAAGTT	GTTCCCGAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGT	CATGTACAAAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTC	3000
AATTATCA	AATTCTTCCC	TCATGCGCTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTGTAC	CAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGC	3120
CTCCAGGGTG	AGGGGCTCG	TCTGCTGGAT	GTACTTGTG	CCGAACTGAG	TGACCCCCCG	3180
GGGCCAGCCG	GTCTGCGAGC	GATTGGCGG	TACACAGAC	ATGCTGGCA	GCTCCGGGGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGCAGGAA	GCCTCGTGC	3300
GAATT						3306

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCGCA	CGAGAAATGGA	TCAACCTCAA	CAACACGTTA	AAAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGTGT	TGCCAGGGAC	AAAGGGCGGT	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTGGAG	TGATGAGAAT	GTTTGGAGC	TAGATAGAAG	TGGTGGTTG	ACACCATTG	240
GGATGTACTA	CCACTTAATT	GTTCACTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAACAAACAG	GATAACATTC	CAACTCTGG	ACATTATCC	TCCCTTCCAT	TTGATGTCAG	360
GCCCGTGT	GAATTCTCAT	CCGGTTTGGT	CTGTCGACTT	AAGATGTGGA	GAAATTAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGT	TAAGGTAGTG	CTTTCTAGG	TTTCCCCCAA	480
ACAATTAAAC	AGATGGATAG	TGGCACCACT	TACGAGATGG	AAAACCAGC	GGAAGGAAGA	540
TTTGGGGAG	AAGTTAAGTT	TGTCTTGGC	CTGTGTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTTAAGT	CTTCAGTGGC	AAACACAA	AACTAGAAAT	GGATCAGAAAT	TTTATCTTG	660
GATGTAAGT	CTCAAGGATG	GTCCTGTCAC	TTCAGTGCT	GTCAGGATG	CAAGATGGC	720
AATCTTTCC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACAACT	CTAGTTCATG	CCTATTGTC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTGTG	GCAATAAATT	CTGCAACGTG	ATGGCGGAC	TCTCGCGCC	CGACGGCCG	900
GACCTGTCT	TGAGGAAGA	GGACCTCCC	TATGAGGAGG	AAATCATGCG	GAACCAATT	960
TCTCGTCAAAT	GTCGCTTCA	TCATCATGAG	TCAACACAGG	GCGCCCGAA	GCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGT	TGACCGACCC	TGCCTATGAA	1140
GATGTCACA	ACTGTATGA	GAGGGCCTT	GTGTTCATGC	ACAAGATGCC	TCGCTGTG	1200
CTAGATTACT	GCCAGTCCCT	CATGGACCA	GGGGCGCTGA	CACACACCC	CCGCACCTTC	1260
GACCGTCCC	TCCGGGCACT	GGCCATCAGC	CAGCACTCTC	GAATTGGCC	CCTGTATCTG	1320
CGCTCCCTGC	GCTCACACCC	ACTGCTGTG	ACGCTGTG	GAGGCTATCG	GCGCTCTCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGGCTG	1440
GATGAGGCCG	CCCAGCGCCT	GGCCACCGTG	GTGAACGAGC	AGCGTTCTG	GTCTAAAGCC	1500
GGCAAGTCCA	ACTACCAGCT	GTGGCACGAG	CTGTCGACCC	TCATCTCCAA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGGGGG	GCTCACCCCG	CTTCACCGAC	1620
CAGCTGGCA	AGCTCTGGT	TTCTCTGCC	GACTACTACA	TCCGCAGCGG	CCATTTGAG	1680
AAGGCTGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGC	GGACTTCACA	1740
CAGGTGTTG	ACAGCTACGC	CCAGTTCGAG	GAGAGCATGA	TCGTGC	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGAGGAGGAT	GATGTGGACC	TGGACGTCG	CCTGGCCCG	1860
TTCGAGCAGC	TCATCAGCCG	GGGCCCGCTG	CTCCCTCAACA	GCGCTTCTG	GCGCCAAAAC	1920
CCACACCCAG	TGACAGGAGC	GGACAAGCGT	GTGCCCTGC	ACCGAGGCCG	CCCCGGGGAG	1980
ATCATCAACA	CCTCACACAGA	GGCTGTGCG	ACGGTGAC	CCTTCAGGC	CACAGGCAAG	2040
CCCCCACACT	TGTGGGTGCG	TTTGTGCAAG	TTTATGAGG	ACAACGGACA	GCTGGAGGAT	2100
GCCCGTGTCA	TCTGGAGAA	GGCCACCAAG	GTGAACCTCA	AGCAGGTGGA	TGACCTGGCA	2160
AGCGTGTG	GTCAGTGC	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCTTG	2220
CGGCTGCTGC	GAAAGGCCAC	GGCGCTGCT	ACCCGGCGG	CCGAGTACTT	TGATGGTCA	2280
GAGCCCGTGC	AGAACCGCGT	GTACAAGTCA	CTGAAGGCT	GGTCCATGCT	CGCCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAGGCGGTG	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCGATGT	TCTGGAGGA	GCACAAAGTAC	2460
TTCGAGGAGA	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAA	TTCATGCCC	GCTATGGGG	CCGCAACGTG	2580
GAGGGGGAC	GGGACCTGTT	TAACAGGCT	CTGGACGGCT	GCCCCC	AAATATGCCAAG	2640
ACCTGTACCC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
CCCGTGTACG	AGCGTGCAC	CAGGGCGCTG	GAGCCCGCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCGA	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCTGCG	TTTGCAGAC	2880
ATGGACTGCA	AGCTCGGGGA	GATTGACCGC	GCCCCGGGCCA	TCTACAGCTT	CTGCTCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGCGCGTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CAGATGCTCA	AGGTCTCGGG	CAGTGCCACG	3120
GGCACCGTGT	CTGACCTGGC	CCCTGGGCG	AGTGGCATGG	ACGACATGAA	GCTGCTGAA	3180
CAGCGGGCAG	ACGAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCCTGCG	CGCCCAGAGC	3240
AAGATCTGT	TCGTGAGGAG	TGACGCCCTC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTCGGCTGGC	GAACGAGAGC	GTGCGAGCCG	CAGTGTGTTG	GAGCCTGAAG	3420
GAAGACTGAC	CGCGCCCTC	GTGCGGAATT	GGCGCACGAGC	AAGACAGCC	CCCAGATCAT	3480
TTGCCTAAA	GGTTTCCCTC	CGAACATCACA	ATATTTCAA	GGAAATCTCAA	ATTTTACAAA	3540
TTTGAAGTG	TGGCATTGG	TGGCCTGTGG	CTGTGTCTC	TCTCTGTAGC	TGTTTCTCC	3600
CTACATCCCT	GAAGGAAGT	TGAGCCTGCT	CCTCCATCCG	CAGACCTCCC	TTTCCAGGGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTC	ACCGTGTCC	TGGCCTCCAG	3720
GCCCCGTGTC	CTCTGTCTC	TGACCCACTA	AGGGCCTGGC	CCATTTGTGC	TAACAGGCA	3780
GTCGGACCTA	GAAGAGCAG	ACAAATCTC	TGGGTACCCA	GTCTGGTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCC	TCTCCCTGC	CCATGTGAAT	TCCCAGGGC	AGAGCCTGAA	3900
ATGTTGACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCCT	3960
CCTGCTGCT	TTCGTGGTT	CAGAGTAGCT	GAGGCTTGTC	TGAGAGGAGT	TGGAGTGTG	4020
TTTTTCACCC	TGGTGGGTG	GCTTTGCTTT	GAGGGCACTT	AGAAAAGCCCA	GCCCAGCCCT	4080
TGCTCTGCC	CTGACACACG	CGGAGCGACT	TTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GCAGCAGGTG	GCATGGAGAC	AAAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCCCGC	4200
TCGGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGCGC	GCCTGCAGGT	CCACACTAGT	GGATCCAAG	AATTCCGGCAC	GAGGAAACT	60
CAACGGTGT	CGAGTGGAGG	ACAGGGACAG	AGCCCTCTGT	GGTGAACCGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAAGTGTCTGA	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGGCA	240
TCTTCCCGGA	ATCAAGATTCA	AAGGATCTCG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTT	GCAGATCACA	GTGCTGGAAAG	CAGGAACCCA	GGCTCAGAGA	GGTGTGCCA	360
GGGGCCAGA	TGCCCTGACA	CTGCTTGAAT	ACACTGAGAC	CCGGAAATCAG	TTCCCTGATG	420
AGCTCATGGA	GCTTGTGATC	TCTCTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCCAGCTGG	CTCCAGCCAT	CCTGCAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGTCTG	AGGATCTGAT	TGGCAAGCTT	ACCAGTCTTC	600
AGCTGCAACA	CCTGTTTATG	ATCCTGCCCT	CACCAAGGTA	TGTGGACCGA	GTGACTGAAT	660
TCCTCCAGCA	AAAGCTGAAG	CAGTCTCCAGC	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAACGAGCA	GGAGGGCACTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAACTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAACGCTG	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCAGCCCTGT	GAACCTGTATG	GGAAACCTCTC	TGTGACACCC	TCCGTGTTCT	TGCCCTGCCA	900
TCTTCTCCGC	TTTGGGATG	AAAGATGATAG	CCAGGGCTGT	TGTTTGGGG	CCCTTCAAGG	960.
CAAAAGACCA	GGCTGACTGG	AAAGTGGAAA	GCCACAGGAA	GGAAACGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAAGA	AGCTGTGGTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAAC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTCT	CGAGAGTACT	1140
TCTAGAGCGG	CCGGGGGCC	ATCGATTTTC	CACCCGGGTG	GGGTAC		1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGAAACAAA	AGCTGGAGCT	CGCGCCGCTG	CAGGTCGACA	CTAGTGGATC	60
GAAAGTTCGT	TACGCAAGC	TCGAAATTAA	CTCTGGCTG	ACCCATAAAC	ATTGCTGA	120

TCTAGGATAT	AGTTGCCTT	CTTGCAGGCA	GCAATCTGGA	TGAGGCCTGG	GAGGCACTGG	180
GTGGCTGCT	GGATCAGGAC	ATCCCAGCG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCC	240
ATCACCCGCA	TCTTATCCAT	GATGGCATTG	GTACCCAGGA	TGTGTACTT	CTTGGAAAGGG	300
TTGGAGGCTG	CATGTTGAT	GGCCCAGTG	GTCTGCCAG	CAGCAGGAG	GCCCACCATC	360
ATCAGAATCT	CACATTCTGC	CTTGCCTTT	GTCACCAACGG	TGCCCCGGAT	ACGCTCACTA	420
AGGGGAAGGT	GCTGGATGAA	GGTAAACCCC	GGGAGGGACAG	AACAGTAGGG	CTCTGCTCTC	480
TGTCCGAAGT	TGAACCTCAC	TGCGCAATT	TTCACCAAGGA	CATGAGGATA	GAGGGCCTGA	540
CCCCCCCAAG	CTTCCTCTG	GATTCGGAAA	GCAATGCCCA	TCCACTTTCC	ATTCTTGTGA	600
AAAGACAGT	CCACGTCAATT	TCCACATTA	AAATCCGAA	AGCAGCCAAT	CACCGGAGAG	660
CTCTGCCGTG	CTAGGAGAGC	GGCTGGGCC	GCAGACTGGG	GGGAAAGCTC	CGCAGCCGCA	720
GTGGGGCCCA	GGATCAGGCC	CCCGCTGGCC	TGGAGAAGCC	CAGTCTGGGC	TGGAGCCTGG	780
GCTGGACAGT	GTGGCCTTC	GTTCGCCCCC	GGGAGCGCTG	CGAGTGTCCG	GGCCTCGGGT	840
GGATTTCGTG	AGCACCAATA	CCTCACGGTT	GCAACACCTGG	GGTTTAGCT	CCCTTGGTTT	900
TAATCCCCTA	GGGGCGGGTG	GGGGCACGGG	AGGAAGGATG	GGCCAGCTGG	GTGCAATCCT	960
GCTGTAAGCC	AGCCATTCTT	TGATTTCTTA	GAATTAACCA	AACGGTCGG	CCGGAGGCCG	1020
CGGGGGCCCG	AGCGGAGCAG	CCCGCGCTGA	GTTCGGCGAG	TCGGCGCTC	GGGGCTGCCG	1080
TCCGCCGCCG	GGACCCCCGGC	CTCTGGCCGC	GGCGCTCCG	GCCTCTGGGG	GGGCCGGGGC	1140
CGCCGGGACA	TGGTGCAGT	CGCACCCCTT	CCCCGCCGCC	GCTGAGCTG	CCGGCCGCCG	1200
CCGGGCTGGG	ACGCTCCGAGC	GGGAAGATGT	TTTCGGCCCT	GAAGAACGTC	GTGGGCTGG	1260
ACCAGGGCCCC	GGGGCGGGAC	AAGAACATCC	CCGCGGGCT	GCAGTCATG	AACCAAGGCGT	1320
TGCAAGGGCG	CTTCGCAAG	GGGGTGCAGT	ACAACATGAA	GATAGTGATC	CGGGGAGACA	1380
GAACACAGGG	CAAGACAGCG	CTGTGGCACC	GGCTGCAGGG	CCGGCGGTT	GTGGAGGAGT	1440
ACATCCCCAC	ACAGGAGATC	CAGGTACCA	GCATCCACTG	GAGCTACAA	ACCACGGATG	1500
ACATCGTAA	GGTTGAAGTC	TGGATGTAG	TAGACAAAGG	AAAATGCAA	AAGCAGGCCG	1560
ACGGCTTAA	GATGGAGAAC	GACCCCCAGG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCCTGGA	CGTGACAAAG	AACTGCAACG	GGGTGGTCAT	GATGTTGCAC	ATTACCAAGC	1680
AGTGGACCTT	CAATTACATT	CTCCGGGAGC	TTCAAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
GCGTCTGGG	GAACATACCGG	GACATGGCG	AGCACCCAGT	CATCTGCCG	GACGACGTGC	1800
GTGACTTCAT	CGAACACCTG	GACAGACCTC	CAGGTTCTC	CTACTTCGG	TATGCTGAGT	1860
CTTCATGAA	GAACAGCTTC	GGGCTTAAGT	ACCTTCATAA	TGTTCAAT	ATCCCATT	1920
TGCAGCTTC	GAGGGAGAGC	CTGTTGCCG	AGCTGGAGAC	GAACAGCTG	GACATGGACG	1980
CCACGCTGG	GGAGCTGTG	GTGCAGCAGG	AGACGGAGGA	CCAGAACTAC	GGCATCTTC	2040
TGGAGATGAT	GGAGGCTCGC	AGCCGTGGCC	ATGCGTCCCC	ACTGGCGGCC	AACGGGCGAGA	2100
GCCCATCCCC	GGGCTCCAG	TCACCACTGC	TGCCCTGCC	CGCTGTGTC	ACGGGGAGCT	2160
CCACGCCCCG	CACACCCAG	CCCGCCCCAC	AGCTGGCCCT	CAATGCTGCC	CCACCATCTT	2220
CTGTGCCCC	TGTACCAACCC	TGAGGCCCC	TGCCCCCACC	TGCGTCCCC	TCAGCCCCG	2280
CCCCACGGCG	CACGATCATC	TCTAGGCTGT	TTGGGACGTC	ACCTGCCACC	GAGGCAGGCC	2340
CTCCACCTCC	AGAGCCAGTC	CCGGCCGCAC	AGGGCCCTGG	AACGGTCCAG	AGTGTGGAGG	2400
ACTTTGTTCC	TGACGACCGC	CTGGACCCCA	GCTTCTGG	AGACACAAC	CCGGCCAGGG	2460
ACGAGAAGAA	GGTGGGGGGC	AAGGTGCCC	AGCAGGACAG	TGACAGTGT	GGGGAGGCC	2520
TGGGGAGGCA	CCCGATGGTG	GCAGGGTTCC	AGGACGATGT	GGACCTCGAA	GACCAAGCC	2580
GTGGGAGTCC	CCCGCTGCC	GCAGGCCCGG	TCCCCAGTC	AGACATCACT	CTTTCGAGTG	2640
AGGAGGAAGC	AGAAGTGGCA	GCTCCCACAA	AAGGCCCTGC	CCCAGCTCCC	CAGCAGTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCTCCATAC	CAGCTCGAA	GCCACGGAGG	GGGACAGCTC	2760
CCACGAGGAC	CGCAGCACCC	CCCTGGCCAG	GGGGTGTCTC	TGTTCGCACA	GGTCCGGAGA	2820
AGCGCAGCG	CACCGAGGCG	CCTCTGTGAGA	TGGAGCCGGG	GAAGGGTAG	CAGGCCCTCT	2880
CGTCCGGAG	TGACCCCCAGG	GGACCCATTG	CTGCACAAAT	GCTGCTTTC	GTCATGGATG	2940
ACCCCGACTT	TGAGAGCGAG	GGATCAGACA	CACAGCGAG	GGCGGATGAC	TTTCCCGTGC	3000
GAGATGACCC	CTCCGATGTG	ACTGACGAGG	ATGAGGGCCC	TGCCGAGCCG	CCCCCACCCC	3060
CCAAGCTCCC	TCTCCCCGCC	TTCAGACTGA	AGAATGACTC	GGACCTCTTC	GGGCTGGGC	3120
TGGAGGAGG	CGGACCCAAG	GAGAGCAGTG	AGGAAGGTA	GGAGGGCAA	ACCCCTCTA	3180
AGGAGAAGAA	AAAAAAACA	AAAAGCTTC	CGAGAGTACT	TCTAGAGCGG	CCGGGGGCC	3240
ATCGATTTT	CACCCGGGTG	GGGTACCA	TAAGTGTAC	CAATTGCC	TATAGTGAGT	3300
CGTATT						3306

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTG GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTCA

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAACACCTATG GTTACAATTG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCGTGTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCTCC GACGCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCACTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCCTGGTCC GCACCAAGTTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAAGGGTC GGGGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCCGTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACCGATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TCGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCGTCTCTC GTCCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCCA CGCACACCA

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC 20

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTCA GAGCGTAGTG 20

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC 20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGGAGAG 20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG 20.

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGAATCTCTG 20

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCCGCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAAG

20

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCA

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTGCG AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACCGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGC GGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACCGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCACTG GTCCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACCGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGAACACAGCG TCTCCCTCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TCCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 378...1799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGATCCAAG GACGCCCCCG CCGACAGGGAG AATTGGTTCC CGGGCCCGCG GCGATGCC	60
CCCGGTAGCT CGGGCCCGTG GTCCGGTGT TGTGAGTGT TCTATGTGGG AGAAGGAGGA	120
GGAGGAGGAA GAAGAACAA CGATTTGTCT TCTCGGCTGG TCTCCCCCGG GCTCTACATG	180
TTCCCCCGAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCTCCCGG GCCCGGATTA	240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CCTTGGATTC AGACGCCGAT TCGCCCCAGTG	300
TTTGGAAAT GGGAAAGTAAT GACAGCTGGC ACCTGAACTA AGTACTTTA TAGGCAACAC	360
CATTCAGAA ATTCAAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT	410
Met Asn Gly Asp Met Pro His Val Pro Ile Thr	
1 5 10	
ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT	458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro	
15 20 25	
CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT	506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Lys Ser Leu Leu Phe Asn	
30 35 40	
GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC	554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp	
45 50 55	
AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTC TCA ACA GAT	602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp	
60 65 70 75	
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC	650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp	
80 85 90	
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC	698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe	
95 100 105	
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTC CAA AGT GGA ATG ATG ATG	746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met	
110 115 120	
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT	794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser	
125 130 135	
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT	842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Arg Phe	
140 145 150 155	
GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT	890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn	
160 165 170	
AGC CCA GTG CCT AGT CCA TAC GCC CCA AGC CCT GCA GGA TAC ATG	938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met	
175 180 185	
CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA	986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln	
190 195 200	

GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser GLY 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCAGCAGGG AACTATGTAG TCACCCCCAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC CAGTTGGCTT CTCTCACTCG CTTCTCCCTG TGGAGAACCC TGTCAGGTG TCACTGCCTC CAGGAAGCTG TCTCTGATTT CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT CGCTCTTGTG CCTGGAATTG TAACCATAGG TTTTCTGTG TCCTGGAGGA CAAGGATGAG	1864 1924 1984 2044 2104

GGCTTCCAC	TTGAGTCTCC	CTGGTGGAGC	CCAGCTCTG	ACATACCTGG	TAAAAGTTCT	2164
CAAGAGAAGA	ACATGGAGGA	GGATGTGGA	TAACAACCC	GGCTGCCTGT	GTGTTCCAAG	2224
CTAGGAAGAT	GTAATGTC	CACAAACGGG	GTAATGGCT	TGCTGCCTC	ACAGCTGTCT	2284
CAAGCCAGG	CCCTGGGCGC	CAGCCCAGC	CCAAGGACTA	GGTCCAGAGC	CACACAGGCC	2344
CAGGCCACAT	CCGCTCACCC	TGGGACCCCT	TGTGGGTAC	AGTCTCCGGC	CCCACCCAGA	2404
CCTCCGTAAAG	GAGAGACCCC	ATGGCAAGGA	CTCAGCCACC	TGCAGTTCA	TAAGCCCCCA	2464
GTGGGTTCTC	AGGCATGAAG	ACCACCGGT	AGAGGCTGAA	CTGGCAGGAA	CCTGTCCTCA	2524
GCCCCCTCTC	ACCCAGCGG	GGCCCTGCT	CAGAGGCGC	ACCCAGGAGC	TGGCCATGAC	2584
CCGTGACTC	CACTCAATCC	CTCTTCTCCA	GGAGCCATGC	AAAGTGTAG	CCAGCCAGGC	2644
CCCTGGAAGG	CAGTCATCAC	CTCTTAAGGC	ATTGTGGGTG	TCGGTCTCTG	AACTGCCAGG	2704
TGCAGCACAC	GACCCGTGTC	CGGTGTTGGA	TAGCAGGGAG	CCATGACCTG	GCAACGATTG	2764
CACAGCTAA	GGGGCACCCG	GGGGGCCCTG	GGTCGGGGCG	GATCAGCTTT	CCCTGGGCAC	2824
ATCTGCTCA	TTCCAGATCT	CCAGGGCTCA	TGTCCTGTGAC	AGGGAGGGAA	GGCTCTGCC	2884
TGGCCTTCCG	TCAGCTCTGC	CACTGAGGC	TGGGAGCCCT	GGGCTTTAGA	GCTGGCTTCT	2944
GCCCCACACTT	TCTCCGTGAA	AGGAAAACAA	CTATGAGTCT	GCCAAACGC	TCTCAGATGC	3004
GTTTTAAAAA	ATTCTGGTCC	CCCGCTCTCG	TCCCATCATC	CGCCTCGGGG	ACTTCCTCTC	3064
TCCCGTGGTC	TCACCCCATCA	TCTGTCACT	GCCACATT	CACCTGGGCC	TGGCCTTTGT	3124
CTCCACCTGA	AACTCCTGAA	AATCTTGAA	TGGATTCTA	GGTCACTGGG	GACTCCGGCA	3184
GCACATCTGG	CTTCAGAATA	AAAGGGCGCC	GGGGTCCCCC	AGCACCTCCC	CAAGCCACAC	3244
CCCTAGCTTC	CCTCCCTATC	CTCTGAGCCT	GAGGGTCCCT	TCAGGCCACC	TTAAGTCCCC	3304
ACCTGGGCTC	CTGCCCCGCC	CCTGGCTAGC	AGCGCCTTCT	CCACCGGGGC	CCCTCTGCT	3364
CACAGAGCCC	CCTCACCTCC	CTGGGGATGA	GGGGCCAGGC	CATGACCTG	AAAGTCTAGC	3424
CCTGGCCTTG	ACCTCCAGG	AGGCCCTCC	CCGGCCCTCTC	CCGGCCCGG	CCCCGTCTC	3484
TGCTGCTGCG	CTCTGGGTG	TGGCCCGAG	ACTGAGCTGC	GCTTGGGGGT	CTGGCGGGC	3544
TGGGCCGTCC	CGCACCGAAC	CCAGCGGTC	GGAGCCCGGC	GGGAAGGC	GAGGTCTTC	3604
TGGGGGCTCC	TCCGACGCC	GAGGGCGCTG	CTTCCCCGGG	CCCGCCCCGG	TTTCTGCGG	3664
AGCCGGGGCC	TCCGCTCTCG	GGTGAACCGG	TGAGACCCCC	GGGGAGGGCC	CTGGGGAGGC	3724
GCGGGCTCTG	CTCCGGGGTC	CCAAACGCAC	TGGCTGCC	TCAGGAGGA	CGCGCACCTC	3784
CACCCACGGG	GCTGGGGCCC	CCACGGCCGC	TCCTCCCGCT	CCCGCAGCCT	GGACGCC	3844
CGAGGGCCG	CCGGGGGCC	CCACGGCCG	CCCCATCCGC	AGGCCAGGAC	TGCTTCCC	3904
GAGCTGGCGG	CCCCCAGCCT	GGAGGAGCCG	GGCCCAGACG	CCCTCCCAGC	CCTCCCCAGC	3964
CCACTCTGGC	CCCGCAGCCC	CCGGCTGGTC	CGAGTGC	TCTCTGGCC	CGGCCTTCC	4024
CGGGGAGGA	AAGAAAAG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Asn	Gly	Asp	Met	Pro	His	Val	Pro	Ile	Thr	Thr	Leu	Ala	Gly	Ile
1				5				10				15			
Ala	Ser	Leu	Thr	Asp	Leu	Leu	Asn	Gln	Leu	Pro	Leu	Pro	Ser	Pro	Leu
				20				25				30			
Pro	Ala	Thr	Thr	Thr	Lys	Ser	Leu	Leu	Phe	Asn	Ala	Arg	Ile	Ala	Glu
					35			40				45			
Glu	Val	Asn	Cys	Leu	Leu	Ala	Cys	Arg	Asp	Asp	Asn	Leu	Val	Ser	Gln
				50			55				60				
Leu	Val	His	Ser	Leu	Asn	Gln	Val	Ser	Thr	Asp	His	Ile	Glu	Leu	Lys
				65			70		75				80		
Asp	Asn	Leu	Gly	Ser	Asp	Asp	Pro	Glu	Gly	Asp	Ile	Pro	Val	Leu	Leu
				85			90				95				
Gln	Ala	Val	Leu	Ala	Arg	Ser	Pro	Asn	Val	Phe	Arg	Glu	Lys	Ser	Met
				100			105				110				
Gln	Asn	Arg	Tyr	Val	Gln	Ser	Gly	Met	Met	Met	Ser	Gln	Tyr	Lys	Leu
				115			120				125				
Ser	Gln	Asn	Ser	Met	His	Ser	Ser	Pro	Ala	Ser	Ser	Asn	Tyr	Gln	Gln
				130			135				140				
Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	Val	Pro	Pro	Gln	Thr
				145			150				155				160
Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	Ser	Pro	Val	Pro	Ser
				165			170				175				
Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	Pro	Tyr	Ser	His	Pro
				180			185				190				
Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	Ala	Ser	Val	Ser	Ser
				195			200				205				

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235 240
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 26...799

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTG AATTGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG Ala Thr Gln Ala Ile Phe Glu Ile Leu	52
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	100
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	148
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	196
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CCG GAC CTC AAA GAA GTA ACT CCT GAA Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	244
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val			
75	80		
GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG	340		
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met			
90	95	100	105
GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT	388		
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys			
110	115	120	
GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA	436		
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys			
125	130	135	
GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC	484		
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly			
140	145	150	
ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA	532		
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly			
155	160	165	
CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC	580		
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro			
170	175	180	185
CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA	628		
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu			
190	195	200	
CCC AGT GGT CTT GGC TGT TCA ACC GTC CTT TCT CCA GAA GGA TCA GCT	676		
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala			
205	210	215	
CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC	724		
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser			
220	225	230	
AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT	772		
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala			
235	240	245	
GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA	826		
Asp Lys Lys Ile Arg Glu Cys Asn Leu			
250	255		
GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGTAA	886		
TTTTAAATTA GAGAACACAA ATAAAATGTA TTAGTGAATA ATAGGTGAGG GTAGGCCAT	946		
TCAGATGCAA GGCCAGCAAT GGGCCTCCCC ATTATCCCCA CCCCCCTTGGT CCCAGTCCCC	1006		
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAGGGTA TTAGACGCAA CATCATGGC	1066		
CCAGGGGAGT CCGAGAAAGAG CTGGCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCTTG	1126		
GTCAGGGAGC ACACCCCAGC CTGAAGAGTG ATGCCATTGG CCAGGGAGTG GTTGGTGTAT	1186		
AGCCGTTGGC TTGAGTGGT AAGGAAAAGA TCTGGGAATG AAGCCCTGTG GCCAGGAAGA	1246.		
TAGACAGGGC AGCAACTCTT GGGCCCTTCAG GCCTCTTCC CACCATAGCA ATGTGGGCAA	1306		
AACTGGTGTG AGGCCCCAGC CAGAAAAAGG AGCCCAAGGC AGAGGGCAAG TGACAAAGGA	1366		
TGTACCATGT CCAATCTCCC ACACCCCTGGG GCTGCCCTTC CCAATGTCCT TCTGTATGAC	1426		
CAAGTTGGC TGGGAGCAGC TCACATGCTC TCTAGCAGGAG AGGGTTCTC AGCTCTGGC	1486		
GGCCGCACTG TGATGTTGA CTGCTGCAGG GTCTGCTCAGA CTCGTTTCTG GTTCCAGCA	1546		
AAGTAGGGCG ACACAGCATT GTGGAAGAGC AGCACGCTCT GTGCTACAC CTTGATCTG	1606.		
TTTCTCTTCA GGAACTTGTG CTGGATGGCC ACATCTCCCC GCAGCTTCTC ATACTTGTC	1666		
CGATGGGCCT GGAAAGTGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGACATCCCGG	1726		
GGGCCTAGAC TCAGCTCCTC TAAGCTGTT CGGTAGGCAT CATATTCCAG CCTGGCAGCC	1786		
TCATACTGT TTACAGCTAT GAGCGTGTCTC TCCATGGCTCT TTGTTGACAA TGTTGTATG	1846		
CTAGAGACAA AGAAGTTCAC GGCTCCTAGC AGCAGTTTCCC CATTCTTCGA TAGTAGTTTC	1906		
TGTGTCTG CATTGAGCC AAATTCCTTC TGAAGCTCTG GGGACTTCTG GCTGAGGTC	1966		
GCAAGGCAAT CACCCAGTGC ATGCTGGTC TGCAAGCAGGC TGAGAGGTG GGCTGTCAGT	2026		
GCCCCGGCCA GCTGCAGGAC ACTCTCATAAC TTGCGCTTCG TCTCACGCG CAACTCAATC	2086		
TGCAGCTCTA GCTCCAGGAT TCCCGCGCCT CCACCTGGTC CCCCCGGGGT CTGCTCTGT	2146		
TGCCATTGGAC GGCATTGTCC CAGATATAGC CGTGGTACA AAGCGGGGAT CTGAGCAGGT	2206		
TTTCTCTACT TGTGCACTA AGCGACGGCTT TATCATGAGC AGCAACTCGG CTTCTGCGAC	2266		
AAACGGAAAT GACAGCAAGA AGTCAAAGG TGACAGCCGA AGTGCAGGGC TCCCCCTCTAG	2326		
AGTGTATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG	2386		

GCTGCCCTT	GGGAAGTCA	CCACCTCCT	GATGCTGAAG	GGGAAAAACC	AGGCCTTCAT	2446
CGAGATGAAC	ACGGAGGAGG	CTGCCAATAC	CATGGTGAAC	TACTACACCT	CGGTGACCCC	2506
TGTGCTGCGC	GGCCAGCCCCA	TCTACATCCA	GTCTCCAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCCC	AACCAGGCGC	GGGCCAGGC	GGCCCTGCAG	GCGGTGAAC	CGGTCCAGTC	2626
GGGGAACCTG	GCCTTGGCTG	CCTCGGCGGC	GCCTGGTGGAT	GCAGGGATGG	CGATGGCCCG	2686
GCAGAGCCCC	GTGCTCAGGA	TCATCGTGGA	GAACCTCTTC	TACCTGTGA	CCCTGGATGT	2746
GCTGCACCG	ATTTCTCCA	AGTTCGGCAC	AGTGTGAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCAGTTC	CAGGGCCCTGC	TGAGTATGC	GGACCCCGTG	AGCCGCCAGC	ACGCCAAGCT	2866
GTCGCTGGAC	GGGCAGAACAA	TCTACAAACGC	CTGCTGCACG	CTGCGCATCG	ACTTTCCAA	2926
GCTCACCGAC	CTCACGTCA	AGTACAACAA	TGACAAGAGC	CGTGACTACC	TCGTGCCGAA	2986
TTCTTGGAT CC						2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

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Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln
      5          10          15
1 Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
      20          25          30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
      35          40          45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
      50          55          60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
      65          70          75          80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Lys Ser Glu
      85          90          95
Ser Gln Cys Arg Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
      100         105         110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
      115         120         125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
      130         135         140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
      145         150         155         160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
      165         170         175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
      180         185         190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
      195         200         205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
      210         215         220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
      225         230         235         240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
      245         250         255
Asn Leu

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(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

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Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
      1          5          10          15

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Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595	600	605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys		
610	615	620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr		
625	630	635
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu		
645	650	655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro		
660	665	670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser		
675	680	685
Thr Ile Pro Ala Pro Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr		
690	695	700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val		
705	710	715
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly		
725	730	735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala		
740	745	750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp		
755	760	765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr		
770	775	780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu		
785	790	795
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu		
805	810	815
Asn Lys Leu Leu Leu Lys Pro Leu Arg Pro His Asn His Pro Leu		
820	825	830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg		
835	840	845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu		
850	855	860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe		
865	870	875
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu		
885	890	895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu		
900	905	910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu		
915	920	925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu		
930	935	940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Val Pro Glu Ile Gln		
945	950	955
Glu Lys Glu Glu Gln Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala		
965	970	975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp		
980	985	990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly		
995	1000	1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg		
1010	1015	1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala		
1025	1030	1035

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro		
1	5	10
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro		
20	25	30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly		
35	40	45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
 50 55 60
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
 65 70 75 80
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
 85 90 95
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
 100 105 110
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
 115 120 125
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
 130 135 140
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
 145 150 155 160
 Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
 165 170 175
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
 180 185 190
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
 195 200 205
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
 210 215 220
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
 225 230 235 240
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
 245 250 255
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
 260 265 270
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
 275 280 285
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
 290 295 300
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
 305 310 315 320
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
 325 330 335
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
 340 345 350
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
 355 360 365
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
 370 375 380
 His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
 385 390 395 400
 Leu Leu Lys Met Asn Phe Thr Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

625 630 635 640
 Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
 645 650 655
 Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
 660 665 670
 Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
 675 680 685
 Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
 690 695 700
 Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
 705 710 715 720
 Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Ser Trp His Thr Pro
 725 730 735
 Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
 740 745 750
 Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
 755 760 765
 Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
 770 775 780
 Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
 785 790 795 800
 Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
 805 810 815
 Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
 820 825 830
 Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
 835 840 845
 Lys

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
 1 5 10 15
 Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
 20 25 30
 Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
 35 40 45
 Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
 50 55 60
 Tyr Lys Leu Trp Tyr Arg Leu Lys Ala Arg Arg Ala Gln Val Lys
 65 70 75 80
 His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
 85 90 95
 Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
 100 105 110
 Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
 115 120 125
 Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
 130 135 140
 Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
 145 150 155 160
 Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
 165 170 175
 Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
 180 185 190
 Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
 195 200 205
 Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
 210 215 220
 Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
 225 230 235 240
 Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
 245 250 255

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
 260 265 270
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
 275 280 285
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
 290 295 300
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
 305 310 315 320
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
 325 330 335
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
 340 345 350
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
 355 360 365
 Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
 370 375 380
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
 385 390 395 400
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
 405 410 415
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
 420 425 430
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
 435 440 445
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
 450 455 460
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
 465 470 475 480
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
 485 490 495
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
 500 505 510
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
 515 520 525
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
 530 535 540
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
 545 550 555 560
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
 565 570 575
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
 580 585 590
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
 595 600 605
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
 610 615 620
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
 625 630 635 640
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
 645 650 655
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
 660 665 670
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
 675 680 685
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
 690 695 700
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
 705 710 715 720
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
 725 730 735
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
 740 745 750
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
 755 760 765
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
 770 775 780
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
 785 790 795 800
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
 805 810 815
 Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
 820 825 830
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835
Leu Lys Glu Asp
850

840

845

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Ser Ala Leu Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
1 5 10 15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
20 25 30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
35 40 45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
50 55 60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
65 70 75 80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
85 90 95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100 105 110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
115 120 125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130 135 140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145 150 155 160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165 170 175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
180 185 190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
195 200 205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
210 215 220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225 230 235 240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
245 250 255
Leu Ser Val Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
260 265 270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
275 280 285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
290 295 300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305 310 315 320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
325 330 335
Pro Pro Ser Glu Ala Leu Pro Pro Ala Cys Pro Ser Ala Pro Ala
340 345 350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
355 360 365
Glu Ala Ala Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
370 375 380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
385 390 395 400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
405 410 415
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
420 425 430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
435 440 445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
450 455 460

Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
465 470 475 480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
485 490 495
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
500 505 510
Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
515 520 525
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
530 535 540
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
545 550 555 560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
565 570 575
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
580 585 590
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
595 600 605
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
610 615 620
Ser Asp Leu Phe Gly Leu Gly Leu Glu Ala Gly Pro Lys Glu Ser
625 630 635 640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
645 650 655
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
660 665 670
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
675 680 685
Tyr Ser Glu Ser Tyr
690